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                  Copyright
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OM protein - protein search, using sw model

May 20, 2005, 10:25:11; Search time 161 Seconds Run on:

(without alignments) 67.263 Million cell updates/sec

US-10-083-576-1 137 1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A_Geneseq_16Dec04:* Database :

geneseqp2002s: *
geneseqp2003as: *
geneseqp2003bs: *
geneseqp2004s: * geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		_	Ade52960 FEN-1 rel	Ada66102 DNAP-rela	Adp12557 Protein e		Aab84854 XPG pepti	Ade52961 FEN-1 rel	Ada66103 DNAP-rela	Ade52962 FEN-1 rel	Ada66104 DNAP-rela	Abr53625.Protein s	Adk64206 Disease t	Adn20626 Bacterial	Abb71879 Drosophil	Abul6227 Protein e	Aau36618 Staphyloc		Abp79659 N. gonorr		Abo81220 Pseudomon	Aab34722 Human sec	Adr10287 Human pro	Aay51120 Human SAR	Adl83102 Human PRO	Abu33976 Protein e
	ID		AD147228	ADE52960	ADA66102	ADP12557	AAO02970	AAB84854	ADE52961	ADA66103	ADE52962	ADA66104	ABR53625	ADK64206	ADN20626	ABB71879	ABU16227	AAU36618	ABM71093	ABP79659	ABB60762	AB081220	AAB34722	ADR10287	AAY51120	ADL83102	ABU33976
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	Query Match Length	1 1 1 1 1 1	29	550	551	1186	135	30	543	543	527	527	493	493	1965	730	978	186	981	336	933	288	474	625	958	958	412
, مد	Query		93.4	93.4	93.4	93.4	86.9	85.8	80.3	80.3	70.1	70.1	41.6	41.6	40.9	39.1	38.0	38.0	38.0	37.2	36.5	35.8	35.8	35.8	35.8	35.8	35.0
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Ado61961 Transcrip Abb63960 Drosophil Adb63920 Bacterial Aab53322 Human col Aab53322 Human col Abb05040 Human NOV Aay99426 Human NOV Aay99426 Human PRO Aab66175 Protein o Aau22196 Human PRO Aab66175 Protein o Aau22196 Human PRO Abb65042 Human PRO Abb65042 Human RRO Abb86175 Human RRO Abb86175 Human RRO Abb86170 Novel hum Abu84435 Human sec Abre66309 Human sec Abre66309 Human sec Abre66309 Human sec Abre66309 Human sec	Human
ADO61961 ABB63960 ADF04901 AAB53322 AAG75073 ABB05041 AAY99426 AAB66175 AAU59196 AAU97038 ABU58572 AAU97038 ABU88435 ABU84435 ABR66309 ABR66309	ABU82878 ABU89999
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# ALIGNMENTS

cancer-specific proliferating cell nuclear antigen; csPCNA; immunoassay; Cancer-specific proliferating cell nuclear antigen binding XPG peptide. Ŕ ADI47228 standard; peptide; 29 27-FEB-2002; 2002US-00083576. 27-FEB-2002; 2002US-00083576. (first entry) indicator; cancer; XPG. MALKAS L H. HICKEY R J. BECHTEL P E. SCHNAPER L. PARK M. HOELZ D J. TOMIC D. US2003162233-A1. Unidentified. 06-MAY-2004 28-AUG-2003 ADI47228; (MALK/) (HICK/) (BECH/) (SCHN/) (PARK/) (HOEL/) (TOMI/) RESULT 1 ADI47228 

Malkas LH, Hickey RJ, Bechtel PE, Schnaper L, Park M, Hoelz DJ; Tomic D;

WPI; 2003-766312/72.

Purification of cancer-specific proliferating cell nuclear antigen, useful for producing antibodies, from a tissue or body fluid sample comprises contacting the sample with an immobilized peptide.

Claim 1; SEQ ID NO 1; 20pp; English.

The invention relates to a novel method for purifying a cancer-specific proliferating cell nuclear antigen (csPCNA) from a tissue or body fluid sample. The novel method comprises contacting the sample with a peptide immobilized on a solid support and isolating the csPCNA from the resulting peptide-csPCNA complex. The purified csPCNA is useful for producing antibodies, e.g. for use in immunoassays, as csPCNA is a good

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Neri BP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention discloses a new composition (I) which comprises a purified flap endonuclease-1 (FEN-1) from e.g. Sulfolobus solfataricus, bytobaculom acrophilum or a chimerical FEN-1 endonuclease having a portion of the above endonuclease in addition to that of Pyrococcus portion of the above endonuclease in addition to that of Pyrococcus northwestian and Aeropyrum permix. Also claimed is a composition comprising a vector having the nucleic acid sequence an isolated nucleic acid sequence encoding the endonuclease mentioned an expect and a vector having the nuclease acid sequence cited above, a composition comprising a host cell and vector cited above, a mixture comprising a first structure-specific nuclease selected from a mixture comprising a first structure-specific nuclease and detecting a target sequence, comprising: (a) providing a sample suspected of containing the target sequence, comprising: (b) providing a sample of forming an invasive cleavage structure in the presence of the target sequence, and a FEN-1 endonuclease selected from the species cited above and (b) exposing the sample to the configuration of the species of the target sequence. The second structure-specific nuclease also comprises a thermostable DNA polymerase. It has a 5.
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diagnostic/prognostic indicator for cancer. This sequence represents the peptide for contacting with the sample on a solid support used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition useful for detecting and characterizing nucleic acid sequences and sequence variants for detecting the presence of viral or bacterial infections or cancer, comprises purified or chimerical FEN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flap endonuclease-1; FEN-1; endonuclease; structure-specific nuclease; invasive cleavage structure; thermostable; DNA polymerase; 5' nuclease viral infection; bacterial infection; cancer; forensic analysis; paternity determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEN-1 related polypeptide used within the scope of the invention, #15.
                                                                                                                                                                                         Gaps
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0
                                                                                                                                        Length 29;
                                                                                                                                                                                       i; Indels
                                                                                                                                      Score 128; DB 7;
Pred. No. 1.1e-11;
1; Mismatches 1;
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                                                                                                                                                                                                                                     1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                              1 LKQLDAQQTQLRIDSFFRLAQQEKEDAK 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (THIR-) THIRD WAVE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                    ADE52960 standard; protein; 550
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17-NOV-2000; 2000US-00714935.
                                                                                                                                           93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-2001; 2001WO-US044953
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                                                                                                                                                                                         Conservative
                                              method of the invention.
                                                                                                                Query Match
Best Local Similarity
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                                                                                            Sequence 29 AA;
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ADES 29-J
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cc wild-type DNA polymerase but retains substantially the same 5' nuclease activity of the wild-type DNA polymerase. The second structure is selected from CLEAVASE BN enzyme, CLEAVASE DN enzyme, CLEAVASE TAThDN enzyme, CLEAVASE TAThDN enzyme, CLEAVASE TATHDN enzyme, CLEAVASE TATHDN enzyme, CC INT and S. cerevisiae Radi/Radio complex. The nucleic acid treatment kit comprises (I) and oligonucleotides capable of forming an invasive cleavage structure in the presence of a target nucleic acid. The conformal portion of the target nucleic acid ond (b) a second oligonucleotide comprise; (a) a first oligonucleotide having a 5' portion complementary to a first portion of the target nucleic acid downstream of and contiguous to the first portion of the target nucleic acid downstream of and contiguous to cligonucleotide comprises a single 3' terminal nucleotide not complementary to the target nucleic acid Administriconally, the kit has a cidifonucleotide comprises a single 3' terminal nucleotides and contiguous to third oligonucleotide complementary to a third portion of the target sequence, the oligonucleotides and candouclease are mixed under conditions where an invasive cleavage structure is formed between the target sequence and the oligonucleotides complementary to a third portion of the target sequence and the oligonucleotides of product. The composition is useful in detecting and characterising complementary as an ener. The composition may also be used in forensic complementary descrete presence of viral or bacterial indetections, and other consisting or few paternity determinations. The sequence presented is a FEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.4%; Score 128; DB 5;
92.9%; Pred. No. 2.5e-10;
iive 1; Mismatches 1;
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2000US-00381212.
2000US-00732622.
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HALL J G.
LYAMICHEV SMITH L M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 550 AA;
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24-MAR-1998;
09-JUL-1999;
08-FEB-2000;
08-DEC-2000;
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(SMIT/)
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Matches
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Lyamichev V, Smith LM;

Hall JG,

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The invention relates to a detection system which has oligomucleotides configured for hybridisation to a target nucleic acid to form an invasive cleavage structure and dendrimer, where the oligomucleotides are attached to the dendrimer. The invention also relates to a method for characterising a nucleic acid sequence comprising providing a sample configured to hybridise to the target nucleic acid, oligomucleotides configured to hybridise to the target nucleic acid, oligomucleotide is configured to hybridise to the target nucleic acid to form an invasive cleavage structure and a dendrimer to which the oligomucleotide is attached, and exposing the sample to the oligomucleotides and an agent comprises a cleavage agent having a structure-specific nuclease. The tecters the presence of an invasive cleavage structure. The agent comprises a cleavage agent having a structure-specific nuclease. The preferably a 5' nuclease comprising an endonuclease or polymerase. The detection system further comprises a spacer molecule, consisting of a carbon chain, polymucleotide or polyglycol, to which the oligomucleotide is attached. The invention is used in the detection and characterisation of nucleic acid sequences and variations in these sequences, used in the converse in the converse of in the converse in the converse converse in the converse converse in the converse converse in the converse c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variation studies. This sequence represents a protein used in the scope
                                                                     Detection system for nucleic acid sequences comprises oligonucleotides configured for hybridizing to target nucleic acid to form invasive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 128; DB 7;
Pred. No. 2.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by mRNA of the invention #167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP12557 standard; protein; 1186 AA
                                                                                                                                                                   Disclosure, Fig 59; 354pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EXPR-) EXPRESSION DIAGNOSTICS INC.
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                                                                                                                     cleavage structure and dendrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2003; 2003WO-US012946.
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20-DEC-2002; 2002US-00325899.
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                       WPI; 2003-596420/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 551 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004042346-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-2004.
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                                                                                     The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; pptide therapy; stem cell growth factor; haematopolesis; tisque growth factor; immunonodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 16862; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                93.4%; Score 128; DB 8; Length 1186; 92.9%; Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 5.8e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 65; SEQ ID NO 2566; 1762pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 16862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO02970 standard, protein; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                              Sequence 1186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAI82901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200164835-A2.
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                   the genes
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening modulator of p15PAF cell cycle protein R0101 activity, by adding a candidate bioactive agent to cell comprising recombinant nucleic acid encoding protein, and determining the agents effect.
          perior cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
peptide therapy. The polypeptides have various cytokine-like activities,
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                        ö
                                                                                                                                                                                   86.9%; Score 119; DB 4; Length 135; 85.7%; Pred. No. 1.2e-09; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p15-PAF cell cycle protein; R0101; mitosis; cell cycle
proliferating cell nuclear antigen; PCNA; cancer; XPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11. .18
/label= PCNA-binding_motif
                                                                                                                                                                                                                                                        1 LKOLDAQOTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2B; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                              AAB84854 standard; peptide; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000; 2000WO-US041296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00420092
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu P, Huang B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XPG peptide fragment.
                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                       Sequence 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                              AAB84854;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Luo Y,
                                                                                                                                                                                                                                                                                                                                       RESULT 6
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Score 117.5; DB 4; Length 30; Pred. No. 4e-10;

85.8%;

Query Match Best Local Similarity

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The invention discloses a new composition (1) which comprises a purified flap endonuclease-1 (FEN-1) from e.g. Sulfolobus solfataricus, flap endonuclease-1 (FEN-1) from e.g. Sulfolobus solfataricus, creation coulom earcophilum or a chimerical FEN-1 endonuclease having a portion of the above endonuclease in addition to that of Pyrococcus corrivoshii and Aeropyrum pernix. Also claimed is a composition comprising a composition comprising a host cell and vector cited above, a composition comprising a host cell and vector cited above, composition comprising a target sequence, comprising a first structure-specific nuclease selected from the species mentioned in composition (1), and a purified second structure specific nuclease and detecting a target sequence, comprising a sample suspected of containing the target sequence, comprising a sample suspected of containing the sample suspected from coligonucleotides capable of forming an invasive cleavage setructure in the prevaiding a sample suspected of containing the sample to the coligonucleotides and FEN-1 endonuclease. The second structure specific cuclease derived from a DNA polymerase. The second structure is cuch that it exhibits reduced DNA synthetic activity from that of the wild-type DNA polymerase. The second structure is celected from CLEAVASE BN thrombin enzyme, CLEAVASE DN enzyme, CLEAVASE D
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition useful for detecting and characterizing nucleic acid sequences and sequence variants for detecting the presence of viral or bacterial infections or cancer, comprises purified or chimerical FEN-1
                                                                                                                                                                                                                                                                                                                                                                                                Flap endonuclease-1; FEN-1; endonuclease; structure-specific nuclease; invasive cleavage structure; thermostable; DNA polymerase; 5' nuclease viral infection; bacterial infection; cancer; forensic analysis; paternity determination.
                                                                                                                                                                                                                                                                                                                                                        FEN-1 related polypeptide used within the scope of the invention, #16
Gaps
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Indels
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1; Mismatches
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                                            1 LKQLDA-QQTQLRIDSFFRLAQQEKEDKR 28
                                                                                         LKOLDAGOGTOLRIDSFFRLAGOEKEDAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaiser MW, Lyamicheva N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                  ADE52961 standard; protein; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-2001; 2001WO-US044953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-NOV-2000; 2000US-00713601.
17-NOV-2000; 2000US-00714935.
                                                                                                                                                                                                                                                                                                              29-JAN-2004 (first entry)
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-750464/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200270755-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyamichev VI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
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  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2002
                                                                                                                                                                                                                                                                 ADE52961;
    Matches
                                                                                                                                                                      RESULT 7
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oligonucleotides comprise: (a) a first oligonucleotide having a 5'

complementary to a first portion of a target nucleic acid and (b)

complementary to a first portion of a target nucleic acid and (b)

complementary to an a 3' portion. The 3' portion of the second

complementary to the target nucleic acid downstream of the second

complementary to the target nucleic acid. Additionally, the kit has a

chird oligonucleotide complementary to a third portion of the target

complementary to the target nucleic acid. Additionally, the kit has a

chird oligonucleotide complementary to a third portion of the target

complementary to the farget sequence, the oligonucleotides and

chird oligonucleotide complementary to a third portion of the target

complementary to the farget sequence, the oligonucleotides and

condouclease are mixed under conditions where an invasive cleavage

structure is formed between the target sequence and the oligonucleotides

condouclease sequence is present in the sample, where the invasive

cleavage structure is cleaved by the endounclease to form a cleavage

product. The composition is useful in detecting and characterising

conducted the presence of viral or bacterial infections, and other

diseases such as cancer. The composition may also be used in forensic

analysis or for paternity determinations. The sequence presented is a FEN

    -1 related polypeptide used within the scope of the invention.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 543 AA;
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Gaps ö Length 543; Score 110; DB 5; Length 57.
Pred. No. 1.2e-07; 3; Mismatches 345 LKHLNAHQTQLRIDSFFRLAQQEKQDAK 372 1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28 80.3%; Query Match Best Local Similarity 78.6' Matches 22; Conservative 셤

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ADA66103 standard; protein; 543 20-NOV-2003 ADA66103; RESULT 8 ADA66103 

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(first entry)

DNAP-related protein #9.

DNAP; invasive cleavage structure; dendrimer; nuclease; endonuclease; polymerase; polyglycol; 5' nuclease; allelic variation.

US2003044796-A1.

06-MAR-2003

27-AUG-2001; 2001US-00940244.

96US-00756386. 98WO-US005809. 99US-00350309. 08-FEB-2000; 2000US-00381212 08-DEC-2000; 2000US-00732622 26-NOV-1996; 24-MAR-1998; 09-JUL-1999;

NERI B P. HALL J G. LYAMICHEV V. (NERI/) NERI

(HALL/) HALL J G. (LYAM/) LYAMICHEV (SMIT/) SMITH L M.

Lyamichev V, Neri BP, Hall JG,

WPI; 2003-596420/56.

Smith LM;

Detection system for nucleic acid sequences comprises oligonucleotides configured for hybridizing to target nucleic acid to form invasive cleavage structure and dendrimer.

Disclosure; Fig 59; 354pp; English

The invention discloses a new composition (I) which comprises a purified flap endonuclease-1 (FEN-1) from e.g. Sulfolobus solfataricus,

Disclosure; SEQ ID NO 144; 871pp; English.

endonuclease

The invention relates to a detection system which has oligonucleotides configured for hybridisation to a target nucleic acid to form an invasive cleavage structure and dendrimer, where the oligonucleotides are attached to the dendrimer. The invention also relates to a method for containing a nucleic acid sequence comprising providing a sample subspected of containing a target nucleic acid, oligonucleotides configured to hybridise to the target nucleic acid to form an invasive cleavage structure and a dendrimer to which the oligonucleotide is cleavage structure and a dendrimer to which the oligonucleotide is cleavage structure and an agent that detects the presence of an invasive cleavage structure. The agent comprises a cleavage agent having a structure specific nuclease, comprises a spacer molecule, consisting of a detection system further comprises a spacer molecule, consisting of a carbon chain, polynucleotide or polyglycol, to which the oligonucleotide carbon chain, polynucleotide or polyglycol, to which the oligonucleotide subsport. The invention is used in the agent are attached to a solid support. The invention is used in the detection and characterisation of nucleic acid sequences and variations in these sequences, used in allalic variation studies. This sequence represents a protein used in the scope ö invasive cleavage structure; thermostable; DNA polymerase; 5' muclease; viral infection; bacterial infection; cancer; forensic analysis; paternity determination. New composition useful for detecting and characterizing nucleic acid sequences and sequence variants for detecting the presence of viral or bacterial infections or cancer, comprises purified or chimerical FEN-1 FEN-1 related polypeptide used within the scope of the invention, #17. endonuclease-1; FEN-1; endonuclease; structure-specific nuclease; Gaps ö Length 543; 3; Indels Score 110; DB 7; Pred. No. 1.2e-07; 3; Mismatches 3; 345 LKHLNAHQTQLRIDSFFRLAQQEKQDAK 372 1 LKOLDAQQTQLRIDSFFRLAQQEKEDKR 28 ż Lyamicheva (THIR-) THIRD WAVE TECHNOLOGIES INC. Ź 3; ADE52962 standard; protein; 527 80.3%; 78.6%; 15-NOV-2000; 2000US-00713601. 17-NOV-2000; 2000US-00714935. 15-NOV-2001; 2001WO-US044953 (first entry) Kaiser MW, Conservative WPI; 2002-750464/81. Local Similarity of the invention Sequence 543 AA; Xenopus laevis. WO200270755-A2 Lyamichev VI, 29-JAN-2004 12-SEP-2002. 22; ADE52962; Query Match Matches RESULT 9 **ADE52962** ઠે 셤 

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portion of the above endonuclease in addition to that of Pyrococus portion of the above endonuclease in addition to that of Pyrococus portion of the above endonuclease in addition to that of Pyrococus an isolated nucleic acid sequence encoding the endonuclease mentioned an isolated nucleic acid sequence encoding the endonuclease encitioned above, a composition comprising a vector having the nucleic acid sequence. CC cited above, a composition comprising a vector having the nuclease selected from the species mentioned in composition (1), and a purified second structure specific nuclease and detecting a target sequence, comprising; (a) providing a sample suspected of containing the target sequence of the target sequence, and a FRN-1 endonuclease selected from c providing a sample suspected of containing the sample to the precise cited above and (b) exposing the sample to the origonucleotides and FEN-1 endonuclease. The second structure in the presence of the target sequence, and a FRN-1 endonuclease selected from comparises a thermostable DNA polymerase. It has a 5.

CC oligonucleotides and FEN-1 endonuclease. The second structure is nuclease derived from a DNA polymerase. The second structure is activity of the wild-type DNA polymerase. The second structure is selected from CLEAVASE BN enzyme, CLEAVASE DN enzyme of the first portion of the farse portion. Complementary to a first portion. The 3' portion of the second conjugonucleotide comprises a single 3' terming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence presented is a FEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid. In detecting a target sequence, the oligonucleotides and endonuclease are mixed under conditions where an invasive cleavage entructure is formed between the target sequence and the oligonucleotides if the target sequence is present in the sample, where the invasive cleavage structure is cleaved by the endonuclease to form a cleavage product. The composition is useful in detecting and characterising specific acid sequences and sequence variants which can be used in detecting the presence of viral or bacterial infections, and other diseases such as cancer. The composition may also be used in forensic
Pyrobaculom aerophilum or a chimerical FEN-1 endonuclease having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related polypeptide used within the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analysis or for paternity determinations.
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Gaps ö Query Match

70.1%; Score 96; DB 5; Length 527;
Best Local Similarity 87.0%; Pred. No. 1.4e-05;
Matches 20; Conservative 1; Mismatches 2; Indels 345 LKQLNAQQTQLRIDSFFRLEQHE 367 1 LKQLDAQQTQLRIDSFFRLAQQE 23 요 8

Sequence 527 AA;

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DNAP; invasive cleavage structure; dendrimer; nuclease; endonuclease; polymerase; polyglycol; 5' nuclease; allelic variation. ADA66104 standard; protein; 527 AA (first entry) DNAP-related protein #10. 20-NOV-2003 ADA66104; 

US2003044796-A1 Xenopus laevis.

The invention relates to a detection system which has oligonucleotides configured for hybridisation to a target nucleic acid to form an invasive cleavage structure and dendrimer, where the oligonucleotides are attached to the dendrimer. The invention also relates to a method for containing a nucleic acid sequence comprising providing a sample comprigured to hybridise to the target nucleic acid, oligonucleotides configured to hybridise to the target nucleic acid to form an invasive cleavage structure and a dendrimer to which the oligonucleotide is cleavage structure and a dendrimer to which the oligonucleotide is cleavage structure. The agent to that detects the presence of an invasive cleavage structure. The agent comprises a cleavage agent having a structure-specific nuclease, comprises a cleavage agent having a structure-specific nuclease, comprises a cleavage agent become molecule, consisting of a detection system further comprises a spacer molecule, consisting of a carbon chain, polynucleotide or polyglycol, to which the oligonucleotide cata support. The invention is used in the agent are attached to a sollid support. The invention is used in the sequences, used in allelic of the invention structure represents a protein used in the scope Detection system for nucleic acid sequences comprises oligonucleotides configured for hybridizing to target nucleic acid to form invasive Lyamichev V, Smith LM; Disclosure, Fig 59; 354pp; English. cleavage structure and dendrimer. 27-AUG-2001; 2001US-00940244. 99US-00350309 2000US-00381212 2000US-00732622 96US-00756386 98WO-US005809 NERI B P. HALL J G. LYAMICHEV V. WPI; 2003-596420/56. Hall JG, SMITH L M of the invention 08-DEC-2000; 08-FEB-2000; 09-JUL-1999; 26-NOV-1996; 24-MAR-1998; 06-MAR-2003 Neri BP, (NERI/) (HALL/) (LYAM/) (SMIT/) 

ö 70.1%; Score 96; DB 7; Length 527; 87.0%; Pred. No. 1.4e-05; Pred. No. 1.4e-05; Multiprotein complex; eukaryote; drug target; diagnosis. 1; Mismatches 345 LKQLNAQQTQLRIDSFFRLEQHE 367 1 LKQLDAQQTQLRIDSFFRLAQQE 23 ABR53625 standard; protein; 493 AA. Protein sequence #SEQ ID 2115. 20-JUN-2003 (first entry) Conservative Saccharomyces cerevisiae. Query Match Best Local Similarity Matches 20; Conserv RESULT 11 **ABR5362**! 셤 ò

EP1258494-A1

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Gaps

Sequence 527 AA;

us-10-083-576-1.rag

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                                                                                                                                                                                                                             The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52508-ABR53003 and ACC6610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not respresented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease or disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                     New isolated protein complexes useful for diagnosing a disease or
                                                                                      Kuester BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
Michon A, Leutwein C, Rick J;
                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                           Disclosure; SEQ ID NO 2115; 17pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                 41.6%; Score 57; DB 6; Length 493;
46.2%; Pred. No. 7.7;
iive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disease treating protein complex-derived protein #1272.
                                                                                     Kruse UD,
                                                                                     Gavin A, Grandi P, Krause R, K)
1, Schultz JD, Superti-Furga GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein complex; drug target; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KOLDAQOTQLRIDSFFRLAQQEKEDK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK64206 standard; protein; 493 AA
                     20-DEC-2001; 2001EP-00130253.
                                          15-MAY-2001; 2001EP-00111774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2001; 2001EP-00130253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 46.2
nes 12; Conservative
                                                                                                                     2003-250078/25.
                                                               (CELL-) CELLZOME AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CELL-) CELLZOME AG
                                                                                                                    WPI; 2003-250078/
N-PSDB; ACC61667.
                                                                                                                                                                                                                                                                                                                                                                              Sequence 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1338608-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
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20-NOV-2002
                                                                                     Bauer A, Ga
Marzioch M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The second protein are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that the specification. The variants are encoded by nucleic acids that conditions. The protein complexes are nactive agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                  New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; card tolerance; beat tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7.7;
5; Mismatches
                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 2543; 13pp; English.
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Best Local Similarity 46.2%;
Matches 12; Conservative 5
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                                                                                                                                                                                                                   disorder in a subject
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HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
WPI; 2003-638460/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003233675-A1.
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(SLAT/)
(CHEN/)
(GOLD/)
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The intention relates to a recomponent DNA construct Comprising a paracterial, where the promoter is positioned to prowide for expression of a polynucleotide encoding a polypeptide from a marcebial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transformed plant where the ceombinant DNA construct and growing the transformed plant where the polymerlectide or polypeptide is useful for improving plant with the recombinant DNA construct is useful for producing plants with improved plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or of the cell cycle pathway with plant growth regulators, increased rate of phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved ligain production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the printed specification but was obtained in electronic forms from from a farch of the printed production but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                 to provide
                                                                                           New recombinant DNA construct comprising a promoter positioned to provious for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                   invention relates to a recombinant DNA construct comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  format from USPTO at segdata.uspto.gov/seguence.html
                Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 42429
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                Chen X,
                                                                                                                                                                           Claim 1; SEQ ID NO 3279; 122pp; English
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                Slater SC,
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2000US-00614150.
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                  Hinkle GJ,
                                                     WPI; 2004-061375/06
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11-JUL-2000;
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                Cao Y,
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                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                 isolated nucleic acid detection reagent for detecting 1000 or more
ss from Drosophila and for elucidating cell signaling and cell-cell
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                        Disclosure; SEQ ID NO 42429; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                  4; Length 730;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #1754.
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                  39.1%; Score 53.5; 1
44.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                              7; Mismatches
Myers EW;
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
 PWD,
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                                                                                                                                                                                                                                                                                                                                            Local Similarity 44.0
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 Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-029926/02.
N-PSDB; ACA20097.
                          WPI; 2001-656860/75
                                        N-PSDB; ABL15982
                                                                                                                                                                                                                                                                                                        Sequence 730 AA;
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                                                                                               interactions.
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 Venter JC,
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                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                  genes
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Matches
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Wall
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the 6113 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide a polypeptide whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding to polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a pene required for underexpressed; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) dentifying the extent of the strains is present in a culture or collection of an organism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) dentifying the target of a compound that inhibits the product is overexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening honologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimuring required for proliferation in cells other than S. aureus, S. typhimuring patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequence is encoded by one of the present did not form part of the printed specification. The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression 

Sequence 978 AA;

Gaps . 9 Query Match

38.0%; Score 52; DB 6; Length 978;
Best Local Similarity 45.5%; Pred. No. 89;
Matches 15; Conservative 2; Mismatches 10; Indels

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Search completed: May 20, 2005, 10:29:27 Job time : 164 secs

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-UUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7956, Ap
7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       (without alignments)
48.609 Million cell updates/sec
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                                                                                                                                May 20, 2005, 10:25:14 ; Search time 43 Seconds
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-940-244-142
US-08-940-244-143
US-09-940-244-144
US-09-246-144
US-09-246-144
US-09-246-1432
US-09-270-767-56735
US-09-270-767-66735
US-09-270-767-61511
US-09-270-767-61511
US-09-252-991A-29966
US-09-543-681A-5186
US-09-543-681A-5186
US-08-695-654-2
US-08-995-654-2
US-08-995-016-10047
US-08-655-352-7
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                                                                                                                                                                                                                    US-10-083-576-1
137
1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                                                                                                                              513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                              Perfect score:
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Database :
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                                                                                                                                Run on:
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Sequence 11627, A Sequence 27821, A Sequence 44900, A Sequence 5203, Ap Sequence 22784, A Sequence 22784, A Sequence 603, App Sequence 1063, App Sequence 1063, App Sequence 11473, A Sequence 11473, A Sequence 11823, Ap Sequence 11823, Ap Sequence 11823, Ap Sequence 11823, Ap Sequence 11272, A Sequence 6012, Ap Sequence 6012, Ap Sequence 20278, Ap Sequence 11823, Ap Sequence 11823, Ap Sequence 6012, Ap Sequence 20278, Ap Sequence 6012, Ap Sequence 20278, Ap		Multiple
US-09-902-540-11627 US-09-252-991A-27821 US-09-621-976-44900 US-09-621-976-5203 US-09-621-976-3895 US-09-621-976-3895 US-09-248-796A-22784 US-09-198-452A-603 US-09-198-452A-603 US-09-198-452A-603 US-09-480-11473 US-09-640-211A-1063 US-09-640-211A-1063 US-09-43-681A-4723 US-09-489-039A-13829 US-09-252-991A-17272 US-09-243-681A-6012	ALIGNMENTS	ucleic Acids By asive Cleavages uite 2200  Version #1.30  5
2 2 3 2 1 1 1 1 1 1 1 4 4 4 4 4 4 4 4 4 4 4 4		RESULT 1 US-08-823-516-142 US-08-823-516-142 Sequence 142, Application US/08823516 Patent No. 5994069 Patent No. 5994069 Patent No. 5994069 Patent Lyamichev, Victor I. APPLICANT: Mat. Andrea L. APPLICANT: Brow, Mary Ann D. TITLE OF INVENTION: Detection Of Nu TITLE OF INVENTION: Detection of Nu TITLE OF INVENTION: Sequential Inva NUMBER OF SEQUENCES: 163 CORRESPONDENCE ADDRESS: ADDRESSEE: Medlen & Carroll, LLP STREET: 220 Montgomery Street, SU CITY: San Francisco CITY: San Francisco STREET: 220 Montgomery Street, SU STREET: 240 Montgomery Street, SU STREET: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBW PC Compatible OPERATION SYSTEM: PC COMPATION OPERATION SYSTEM: PC COMPATION OPERATION DATA: APPLICATION NUMBER: PCT/US97/0107 FILING DATE: 21-JAN-1997 PRIOR APPLICATION NUMBER: US 08/759,038 FILING DATE: APPLICATION DATA: APPLICATION NUMBER: US 08/759,314 FILING DATE: 02-DEC-1996 PRIOR APPLICATION NUMBER: US 08/759,386
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	·	RESULT 1 US-08-823-516-142 IS-08-823-516-142 Sequence 142, Application US/0 Patent No. 594069 Patent No. Mary Ann TITLE OF INVENTION: Sequen NUMBER OF SEQUENCES: 163 CORRESPONDENCE ADDRESS: 63 CORRESPONDENCE ADDRESS: 62 PADRESSEE: Medlen & Cart STREET: 220 Montgomery STREET: 220 Montgomery STREET: 220 Montgomery STREET: 220 Montgomery STREET: 216 formia COUNTRY: United States OSTATE: Glifornia COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compati OPERATING SYSTEM: PC-10S SOFTWARE: Patent Relea CURRENT APPLICATION DATA: APPLICATION NUMBER: US/OFILING DATE: 02-DEC-1996 PRICH APPLICATION NUMBER: US/OFILING DATE: 29-NOV-1996 PRICH DATE: 29-NOV-1996
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		

NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: FORS-02736

Sequence

Sequence

Sequence

Sequence

US-09-198-452A-171 US-09-438-185A-152 US-09-270-767-60370

Sequence

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:YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 22; Conserv
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Patent No. 5994069

GENERAL INFORMATION:
APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: Sequential Invasive Cleavages
NUMBER OF SEQUENCES: 163
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisc
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·,
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                                                                                                                                                                                                                                   DB 2; Length 550;
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                                                                                                                                                                                                                                   Score 128; DB 2;
Pred. No. 3e-11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 128; DB 4;
Pred. No. 3e-11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Neri, Darce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
APPLICANT: Applicant: Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PatentIn version 3.1
SEQ ID NO 142
LENGTH: 550
                                                                                                                                                                                                                                                                                                                                                   345 LKOLDAOOTOLKIDSFFRLAOOEKEDAK 372
                                                                                                                                                                                                                                                                                                               1 LKOLDAQOTOLRIDSFFRLAQOEKEDKR 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 142, Application US/09940244
Patent No. 6692917
GENERAL INFORMATION:
                TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 550 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
TOPOLOGY: not relevant
TOPOLOGY: procein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.4%;
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 92.9%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 92.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-940-244-142
                                                                                                                                                                                               US-08-823-516-142
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US-08-823-516-143
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Gaps
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Pred, No. 1.6e-08;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110; DB 2; Length 543;
Pred. No. 1.6e-08;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Neri, Bruce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REPERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: Patentin version 3.1
SEQ ID NO 143
LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 LKHLNAHQTQLRIDSFFRLAQQEKQDAK 372
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                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,314
PILING DATE: 02-DEC-1996
FILING DATE: 29-NOV-1996
PRIOR APPLICATION NUMBER: US 08/756,386
PRIOR APPLICATION NUMBER: US 08/756,386
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
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US/08/823,516
24-MAR-1997
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; Sequence 143, Application US/09940244
; Patent No. 6692917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS.
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 143:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS: not relevant
not relevant
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78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.3%;
Best Local Similarity 78.6%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-09-940-244-143
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STRANDEDNESS: no
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345 LKQLNAQQTQLRIDSFFRLEQHE 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-940-244-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 144
LENGTH: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                         APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Mast, Andrea L.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
TITLE OF INVENTION: Sequential Invasive Cleavages
CORRESPONDENCE: 163
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.1%; Score 96; DB 2; Length 527; 87.0%; Pred. No. 2e-06; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR.1997
CLASSIFICATION NUMBER: PCT/US97/01072
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/92/01072
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,314
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/756,386
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 22-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-ULL-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING BATE: 12-ULL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
                                               1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02736
                                                                                                                                                                                       Sequence 144, Application US/08823516
Patent No. 5994069
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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Best Local Similarity 87.0*
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                                                                                                                                                                 US-08-823-516-144
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US 60/94,725

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NOS: 28208
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.1%; Score 96; DB 4; Best Local Similarity 87.0%; Pred. No. 2e-06; Matches 20; Conservative 1; Mismatches
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Pred. No. 1.7;
Sequence 144, Application US/09940244

Patent No. 6692917
GENERAL INFORMATION:
APPLICANT: Neri, Bruce P.
APPLICANT: Lyamichev, Victor
APPLICANT: Lyamichev, Victor
APPLICANT: Expension Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244

CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422

SOFTWARE: PatentIn version 3.1
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; Patent No. 6747137
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; ORGANISM: Candida albicans
US-09-248-796A-19321
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Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Xenopus laevis
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Fri May 20 11:21:18 2005

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Query Match
Best Local Similarity
Matches 11; Conserva
        Best Local Similarity
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US-09-252-991A-29966
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                                                Matches
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| Retent No. 683347
| GENERAL INFORMATION:
| APPLICANT: Goldman. Barry S.
| APPLICANT: Goldman. Barry S.
| APPLICANT: Goldman. Steven C.
| APPLICANT: Miseand Roger C.
| APPLICANT: Wiseand Noger C.
| APPLICANT: Wiseand Noger C.
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
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| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof:
| TILLE OF INVENTION: Myacoccus xanthus Yanthus Ya
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILER REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41511
LENGTH: 336
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                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-56735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Xaa means any amino acid US-09-270-767-41511
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SSOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56735
LENGTH: 121
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                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Drosophila melanogaster
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 44.0
Matches 11; Conservative
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| Sequence 22837, Application US/09248796A
| Patent No. 6747137
| GENERAL INFORMATION:
| APPLICANT: Keith Weinstock et al
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN.
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| FILE REFERENCE: 107196.132
| FILE REFERENCE: 107196.132
| CURRENT FILING DATE: 1999-02-12
| PRIOR FILING DATE: 1998-02-13
| PRIOR FILING DATE: 1998-02-13
| PRIOR FILING DATE: 1998-08-13
| PRIOR FILING DATE: 1998-08-13
| SEQUENCE OF SEQUENCE: 1998-08-13
| SEQUENCE: 1998-08-13
| SEQUENCE: 1998-08-13
| SEQUENCE: 1998-08-13
| SEDENCE: 1998-08-13
| SEQUENCE: 1998-08-13
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29966
LENGTH: 288
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Pred. No. 29;
5; Mismatches
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Similarity 38.5%; Pred. No. 13; 10; Conservative 7; Mismatches
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                                                                                                                         163 RMDAORROHEAEQLRRLAOOOEAESR 188
                                                                            3 QLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                               Sequence 29966, Application US/09252991A Patent No. 6551795
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; Sequence 5186, Application US/09543681A
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illarity 40.7%;
Conservative
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19 QQKELQIDS---LLQQEKE 34
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ADDRESSEE: INCYTE PH
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US-08-700-178-2
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                     GENERAL INFORMATION:

APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5186
LENGTH: 478
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APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: HYALURONNAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
NUMBER OF SEQUENCES:
ADDRESSE: NOTHE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 4; Length 478; Pred. No. 45;
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STREET: 3174 PORTER DEIVE
CITY: PAIO Alto
STATE: COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COM
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FILING DATE: 10-MAR-1995
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0028US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 AQQTQINSDKFYQKLEEHEWDR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AQQTQLRIDSFFRLAQQEKEDK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08402217A
Patent No. 5587301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 34.3%;
Similarity 36.4%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Proteus mirabilis
US-09-543-681A-5186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.9
Best Local Similarity 63.2
Matches 12; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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Best Local Similarity
Matches 8; Conserva
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                                                                                   APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Sellhamer, Jefferey J.
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,178
FILING DATE: August 20, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,217
FILING DATE: March 10, 1995
ATTORNEY/ASTRI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46.5; DB; Pred. No. 38; 2; Mismatches
                                                                                                                                                                                                                                         E: INCYTE PHARMACEUTICALS, INC. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0028-1 DIV
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                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 2, Application US/08700178
Patent No. 5783669
Patent No. 5783669 5700912
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 QQTQLRIDSFFRLAQQEKE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 QQKELQIDS---LLQQEKE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 351 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.2<sup>3</sup>
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-700-178-2
                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
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Gaps

Э,

2; Indels

2; Mismatches

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
            Copyright
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OM protein - protein search, using sw model

May 20, 2005, 10:25:10 ; Search time 16 Seconds Run on:

(without alignments) 168.379 Million cell updates/sec

1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28 US-10-083-576-1 137 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	gene BRCCS protein	epair	u	DNA repair protein	hypothetical prote	GLO3 protein - yea	probable proteasom	conserved hypothet	lipopolysaccharide	hypothetical prote		hypothetical prote	F9L1.15 protein -	probable periplasm	hypothetical prote		cal	•~	hypothetical prote		hyaluronan recepto	gene Tcp-1x protei	hypothetical prote	integrases homolog		t complex polypept	T-complex protein	methyl-accepting c	probable membrane
SUMMARIES	ID	IS8009	835993	A57650	S35994	F86263	S50625	T41014	B89971	S61299	S44507	B83430	140597	B86286	A81282	T22037	AG2503	T13692	T36717	T31555	Н96622	JC5016	A48911	T16935	AE1758	S10486	JC1443	JQ0866	AB1940	AF1047
	DB		7	7	~	7	7	~	7	7	~	7	N	7	7	7	7	7	7	7	7	ч	7	7	7	~	7	~	7	7
	Length	1185	1186	1170	1196	492	493	129	978	336	355	276	355	1451	189	229	238	385	613	1400	1469	725	39	345	384	256	256	256	1102	1108
do	Query Match	93.4	93.4	80.3	70.1	43.8	41.6	38.7	38.0	37.2	36.5	35.8	35.8	35.8	35.0	35.0	34.3	34.3	34.3	34.3	34.3	33.9	33.6	٠	•	ë.	•	33.6	•	33.6
	Score	128	128	110	96	9	57	53	52	51	20	49	49	49	48	48	. 47	47	47	47	47	46.5	46	46	46	46	46	46	46	46
	Result No.		7	m	4	D.	9	7	80	٠ م	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24			27		29

probable tripeptid hypothetical prote hypothetical prote involucrin - orang conserved hypothet hypothetical prote neurocalcin beta - neural visinin-lik ADP-heptose-LFS he lippolysaccharide ctefin - fruit fly t-complex-type mol CT147 hypothetical	conserved hypothet	hypothetical prote
739249 726205 726205 726205 757441 749496 749105 7401073 881869 873360 813163 86509	C81558 H72112	T00298
00000000000000	0 0	7
1274 374 4114 835 963 1087 1191 336 336 406 556	1537	167
	32.8	32.5
44444 NONNN 4444444 ONNNNNNNNNNNNN	4, 4, N N	44.5
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ALIGNMENTS

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C. Accession 158000
C. Accession 158000
C. Accession 158000
C. Accession 158000
Mutat. Res. 314, 167-175, 1994
A. Title: An ERCC5 gene with homology to yeast RAD 2 is involved in group G xeroderma pignare reference number: 158009; MUID:94173288; PMID:7510366
A. Accession: 158009
A. Accession: 158009
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
A. Molecule with a mRNA
A. Accession: 158009
                                                                                                     Č;Species: Ĥomo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1185 <RES>
A;Cross-references: GB:D16305; NID:g303606; PIDN:BAA03812.1; PID:g303607
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: GDB:ERCC5
A,Cross-references: GDB:120515; OMIM:133530
A,Map position: 13q33-13q33
                                                                  gene ERCC5 protein - human
RESULT 1
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Gaps ö Score 128; DB 2; Length 1185; Pred. No. 2.4e-10; indels 0 93.4%; Query Match Best Local Similarity 92.9° Matches 26; Conservative

ö

1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28 g ò

RESULT 2

DNA repair protein XPGC - human N;Alternate names: xeroderma pigmentosum group G complementing factor; XP-G factor C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004 C;Accession: S35993; S33319; Ā54439; I39304

submitted to the EMBL Data Library, January 1993 A,Reference number: 835993 A,Accession: 835993

A; Molecule type: mRNA A; Residues: 1-1186 < CLAA. A; Residues: 1-1186 < CLAA. A; Cross-references: UNIPROT: P28715; EMBL: X69978; NID: 9298110; PID: 9298111 R; Scherly, D.; Nouspikel, T.; Corlet, J.; Ucla, C.; Bairoch, A.; Clarkson, S.G. Rature 363, 182-185, 1993 A; Title: Complementation of the DNA repair defect in xeroderma pigmentosum group G cells A; Reference number: 833319; MUID: 93247645; PMID: 8483504

A; Accession: S33319

A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-95,753-889,1166-1186 <SCH> A;Cross-references: EMBL:X69978

```
hypothetical protein F13K23.23 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 (Species: F86263 R). Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chony, M.F.; Hudbes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000 A. Fullian, J. J.; Jehkins, J. J.; Jehkins, J. Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Squence and analysis of chromosome 1 of the plant Arabidopsis.
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NyAlternate names: protein YER122c
C;Species: Saccharomyces crevisiae
C;Species: Saccharomyces crevisiae
C;Date: 28-Jan-1995 #sequence revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S50625; 847007; $50036
R;Diecrich, F.S.
R;Diecrich, F.S.
A;Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda c A;Reference number: S50625
               A,Accession: 335994
A,Accession: 355994
A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Rosidues: 1-1196 <CLAA
A,Crose_references: UNIPROT:P14629; EMBL:X69977; NID:g312432; PID:g312433
A,Fitcherly, D.; Nouspikel, T.; Corlet, J.; Ucla, C.; Bairoch, A.; Clarkson, S.G.
Nature 363, 182-185, 1993
A,Fitle: Complementation of the DNA repair defect in xeroderma pigmentosum group G cells
A,Reference number: 33319; MUID:93247645; PMID:8483504
A,Accession: S33320
A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
A,Rosidues: 1-95,786-922,1176-1196 <SCH>A,Rosidues: 1-95,786-922,1176-1196 <SCH>C;Reywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9LPV2; GB:AE005172; NID:g8698744; PIDN:AAF78502.1; GSPDB:GNC
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 70.1%; Score 96; DB 2; Length 1196; Local Similarity 87.0%; Pred. No. 1e-05; nes 20; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 43.8%; Score 60; DB 2; Length 492; 1 Similarity 50.0%; Pred. No. 0.66; 13; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1014 LKQLNAQQTQLRIDSFFRLEQHE 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LKQLDAQQTQLRIDSFFRLAQQE 23
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Matches 13; Conserv
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A; Residues: 1-493 <DIE>
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A;Status: preliminary
A;Molecule type: DNA
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Matches
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R;MacInnes, M.A.; Dickson, J.A.; Hernandez, R.R.; Learmonth, D.; Lin, G.Y.; Mudgett, J.S Mod. Cell. Biol. 13, 6393-6402, 1993
A;Title: Human BRC5 CDNA-cosmid complementation for excision repair and bipartite amind A;Reference number: A54439; WUID:94019313; PMID:8413238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repair protein XPG - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A5-7650
R;Harada, Y.N.; Matsuda, Y.; Shiomi, N.; Shiomi, T.
Genomics 28, 59-65, 1995
A;Title: Complementary DNA sequence and chromosomal localization of xpg, the mouse count A;Reference number: A57650; MUID:96070433; PMID:7590748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A57650
A;Status: preliminary
A;Noteule type: mRNA
A;Noteule type: mRNA
A;Residues: 1-1170 cHRN>
A;Cross-references: UNIPROT:P35689; GB:D16306; NID:g1389576; PIDN:BAA03813.1; PID:d10043
C;Genetics:
A;Genetics:
A;Genetics: xpg
C;Keywords: DNA repair
                                                                                                                                          A; Accession: A54439
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
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A; Residues: 1-253, W. 255-1103, D', 1105-1186 < WAC>
A; Cross-references: GB:L20046; NID:g306741; PIDN:AAC37533.1; PID:g306742
A; Cross-references: GB:L20046; NID:g306741; PIDN:AAC37533.1; PID:g306742
A; Cross-references: GB:L20046; NID:g306741; PIDN:AAC37533.1; PID:g306742
A; Mole: nucleotide sequence nor conceptual translation is complete
R; Samec, S; Jones, T.A.; Corlet, J.; Scherly, D.; Sheer, D.; Wood, R.D.; Clarkson, S.G. Genomics 21, 283-285, 1994
A; Title: The human gene for xeroderma pigmentosum complementation group G (XPG) maps to A; Reference number: 139304; MUD:94375034; PMID:808806
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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DNA repair protein XPGC - African clawed frog
DNA repair protein XPGC - African clawed frog
C;Species: Kenopus laevis (African clawed frog)
C;Dete: 03-Mar-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S35994; S33320
R;Clarkson, S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-88 <RES>
A;Cross-references: EMBL:X71341; NID:9495253; PIDN:CAAS0481.1; PID:9825732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 110; DB 2; Length 1170;
Pred. No. 9.5e-08;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKOLDAQOTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GDB:120515, OMIM:133530
A,Map position: 13q33-13q33
A,Introns: 30/1
A,Note: the list of introns is incomplete
C,Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.3%;
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nes 22; Conservative
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Query Match

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AkGene: GDB:ERCC5; ERCM2 AkCross-references: GDB:1

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Genetics:

A;Molecule type: DNA

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Indels

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A;Residues: 1-978 <KUR>
A;Residues: 1-978 <KUR>
A;Cross-references: UNIPROT:Q99T35; GB:BA000018; PID:g13701636; PIDN:BAB42929.1; GSPDB:c
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipopolysaccharide heptosyltransferase (EC 2.4.99.-) II rfar [similarity] - Neisseria gc C:Species: Neisseria gonorrhoeae C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C;Accession: S61299 R;Schwan, E.T.; Robertson, B.D.; Brade, H.; van Putten, J.P.M. A;Accession: S12, 267-275, 1995 A;Title: Gonococcal rfar mutants express Rd(2) chemotype LPS and do not enter epithelial A;Reference number: S61299; MUID:95264913; PMID:7746148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Redidues: 1-336 <SCH>
A;Redidues: 1-336 <SCH>
A;Cross-references: UNIPROT:Q51063; EMBL:Z37141; NID:g59919; PIDN:CAA85504.1; PID:g5995
A;Orce: the sequence of residues 1-2 are not shown in this paper
C;Superfamily: ADP-heptose-LPS heptosyltransferase II
C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                Score 52; DB 2; Length 978;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAQLKEEATQLEPVKQSDIDAFISLNQQENEIK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LKQLDAQQTQLR-----IDSFFRLAQQEKEDK 27
                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.2%;
                                                                                                                                                                                                                                                                                                ch 38.0%;
1 Similarity 45.5%;
15; Conservative ;
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Best Local Similarity 42.3%;
Matches 11; Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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A;Residues: 1-355 <POD>
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A;Cross-references: UNIPROT:P38682; EMBL:U18916; NID:g1384128; PIDN:AAC03220.1; PID:g603
R;Ireland, L.S.; Johnston, G.C.; Drebot, M.A.; Dhillon, N.; DeMaggio, A.J.; Hoekstra, M.
EMBO J. 13, 3812-3821, 1994
A;Title: A member of a novel family of yeast 'Zn-finger' proteins mediates the transitic
A;Reference number: S47007
A;Molecule type: DNA
A;Redesion: S47007
A;Molecule type: DNA
A;Redidues: 1-221, C', 223-405, 'VSA' <IRE>
A;Cross-references: EMBL:X79514
R;Hockstra, M.F.
Submitted to the EMBL Data Library, June 1994
A;Reference number: S50036
A;Molecule type: DNA
A;Residues: 1-221, C', 223-405, 'GSA' <HOE>
A;Cross-references: EMBL:X79514; NID:g510448; PIDN:CAA56046.1; PID:g510449
A;Residues: SGD:S0000924; MIPS:YER122C
A;Gnetics:
A;Gnet SGD:GLO3
A;Cross-references: SGD:S0000924; MIPS:YER122C
A;Map position: 5R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable proteasome maturation factor - fission yeast (Schizosaccharomyces pombe) (Species: Schizosaccharomyces pombe) (Species: Schizosaccharomyces pombe) (Species: Schizosaccharomyces pombe) (Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 (Shacession: T41014 (Species) (September 1998 (Species) (September 1998 (Species) (September 1998 (Species) (Specie
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Pred. No. 1.6;
6; Mismatches 8; Indels
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hes 13; Conservative
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A,Map position: 3
A,Introns: 78/3
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Matches 12; Conserv
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A;Status: preliminary
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Best Local &
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hypothetical protein, 41.2K (insertion sequence IS1186) - Bacteroides fragilis C;Species: Bacteroides fragilis C;Species: Bacteroides fragilis C;Date: 16-Feb-1995 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004 C;Accession: 844507; 834201 R;Podglajen, I:, Breuil, J:, Collatz, E. R,Podglajen, I:, Breuil, J:, Collatz, E. A,Title: Insertion of a novel DNA sequence, IS1186, upstream of the silent carbapenemase A,Reference number: $44507; MUID:94335620; PMID:8057831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q08536; EMBL:X72301; NID:g313686; PIDN:CAA51049.1; PID:g3136
C;Genetics:
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B83430
hypothetical protein PA1714 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                     Gaps
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Score 51; DB 2; Length 336;
Pred. No. 8.9;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 355;
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192 KDVDARWTEKRGDTFYGYKQHVKVDK 217
                                                                                                        1 LKQLDAQQTQLRIDSFFRLAQQEKED 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Mobile element: insertion sequence IS1186
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us-10-083-576-1.rpr

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A; Cross-references: UNIPROT: Q9X148; GB: AEO05172; NID: g5103820; PIDN: AAD39650.1; GSPDB: GN(
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42.9%;
                                                                                                                                               Query Match 35.8%;
Best Local Similarity 39.1%;
Matches 9; Conservative
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Best Local Similarity 42.9
Matches 12; Conservative
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A;Accession: T22037
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A;Molecule type: DNA
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F911.15 protein - Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004
C;Accession: B86286
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Atterence number: A86141; MUID:21016719; PMID:11130712
A;Accession: B86286
A;Scteuce type: DNA
A;Residues: 1-1451 <STO>
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hypotherical protein A (IS1168) - Bacteroides vulgatus

hypotherical protein A (IS1168) - Bacteroides vulgatus

c;Species: Bacteroides vulgatus

c;Species: Bacteroides vulgatus

c;Species: Bacteroides vulgatus

c;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004

C;Accession: I40597; S39333

R;Haggoud, A.; Reysset, G.; Azeddoug, H.; Sebald, M.

Antimicrob. Agents Chemcher. 38, 1047-1051, 1994

Antimicrob. Agents Chemcher. 38, 1047-1051, 1994

Antimicrob. Agents Chemcher. 140183; MUID:94346804; PMID:8067736

A;Reference number: I40183; MUID:94346804; PMID:8067736

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <RES>

A;Cross-references: UNIPROT:Q45799; EMBL:X71444; NID:9435262; PIDN:CAA50579.1; PID:94352

A;Cross-references: UNIPROT:Q45799; EMBL:X71444; NID:9435262; PIDN:CAA50579.1; PID:94352
                                                                                          M.J.; Br
K.; Lim,
                                                                                                                                                                                                        A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A; Reference number: A82950; MUD:20437337; PMID:10984043
A; Accession: B83430
A; Accession: B83400
A; Status: preliminary
A; Molecule type: DNA
A; Residuae: 1-276 < STOO
A; Cross-references: UNIPROY: 091321; GB:AE004598; GB:AE004091; NID:g9947687; PIDN:AAG0510
A; Experimental source: strain PA01
                                                                                       P.; Hickey,
A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                     C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: B83430 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicl addman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larl.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 18;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 2; Length 276;
Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
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   C; Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.8%;
ilarity 43.3%;
Conservative
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Best Local Similarity 42.3%;
Matches 11; Conservative
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tes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Genetics:
A,Gene: PA1714
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probable periplasmic protein Cj1372 [imported] - Campylobacter jejuni (strain NCTC 11168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: A81282
C;Accession: A81282
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrelli
Akture 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypel
A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:Q9PMS8; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73799:
A,Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q20231; EMBL:Z69302; PIDN:CAA93265.1; GSPDB:GN00020; CESP:F41
A;Experimental source: clone F40F8
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22037
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A;Introns: 25/1; 61/3; 105/3; 126/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F40F8.3
C;Genetics:
A;Map position: 1
C;Superfamily: ATP-binding cassette homology; chromobox homology
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A;Molecule type: DNA
A;Residues: 1-229 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;MacDougall, R.
submitted to the EMBL Data Library, February 1996
                                                                                                       DB 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.0%; Score 48; DB ilarity 29.6%; Pred. No. 16; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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Pred. No. 13;
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                                                                                                                   Score 49;
Pred. No.
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Search completed: May 20, 2005, 10:26:38 Job time : 17 8ecs

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51, Appl
143, App
143, App
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143, App
144, App
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4.866 Million cell updates/sec
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Sequence 5
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cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-033-297-142
US-10-290-386-142
US-10-356-861-142
US-10-897-793-142
US-10-897-793-143
US-10-341-434-143
US-10-033-297-143
US-10-033-297-143
US-10-290-386-143
US-10-290-386-143
US-10-897-793-143
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                  US-10-083-576-1
137
1 LKQLDAQOTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                                     1434725 seqs, 334507595 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*
                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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128
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Sequence 144, App
Sequence 144, App
Sequence 145, App
Sequence 1451, App
Sequence 1211, A
Sequence 1211, A
Sequence 1211, A
Sequence 166573,
Sequence 166573,
Sequence 22116, A
Sequence 22116, A
Sequence 61900, A
Sequence 61900, A
Sequence 862, App
Sequence 862, App
Sequence 173364,
Sequence 173364,
Sequence 173364,
Sequence 173364,
Sequence 173364,
Sequence 16, App
Sequence 16, App
Sequence 16, Appl
                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
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0 US-09-940-244-144
3 US-10-290-386-144
5 US-10-290-386-144
6 US-10-356-861-144
6 US-10-356-861-144
6 US-10-36-861-144
6 US-10-36-9493-3279
5 US-10-36-9493-3279
6 US-10-767-701-58982
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6 US-10-767-701-47463
6 US-09-925-299-862
7 US-09-925-299-862
8 US-10-425-114-52116
9 US-09-925-299-862
0 US-09-925-299-863
0 US-09-863-776-18
0 US-09-863-776-18
0 US-09-863-776-18
0 US-09-863-776-20
0 US-09-863-776-20
0 US-09-863-776-20
0 US-09-863-776-20
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Sequence 142, Application US/09940244

Publication No. US20030044796A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION: NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PatentIn version 3.1
SEQ ID NO 142
LENGTH: 550 CRGANISM: Homo sapiens US-09-940-244-142 JS-09-940-244-142

ö Query Match 93.4%; Score 128; DB 10; Length 550; Best Local Similarity 92.9%; Pred. No. 2.8e-10; Matches 26; Conservative 1; Mismatches 1; Indels (

ö

Gaps

US-10-033-297-142; Application US/10033297; Sequence 142, Application US/020020187486A1; GENERAL INFORMATION: APPLICANT: Hall, Jeff G.

Sequence 1 Sequence 1 Sequence 1

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### PEPLICANT: Lukowatak, Andrew A.

### TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences
### FILE REPERENCE: FORS-07459
### CURRENT PAPLICATION NUMBER: US/10/290,386
### CURRENT FILING DATE: 2002-11-07
### PRIOR APPLICATION NUMBER: 60/344,946
### PRIOR PRILING DATE: 2001-11-07
### PRIOR PRILING DATE: 2001-11-07
### PRIOR PRILING DATE: 2001-11-12
### PRIOR PRILING DATE: 2001-11-12
### PRIOR PRILING DATE: 2001-11-12
### PRIOR PRILING DATE: 2000-02-08
### PRIOR PRILING DATE: 1999-07-09
### PRIOR PRILING DATE: 1996-07-12-02
### PRIOR PRILING DATE: 1996-07-12-02
### PRIOR PRILING DATE: 1996-11-26
### PRIOR PRILING DATE: 1996-11-26
### PRIOR PRILING DATE: 1996-07-12
### PRIOR PRILING DATE: 1996-01-24
### PRIOR PRILING D
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92.9%;
   Lukowiak, Andrew A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic US-10-290-386-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.9
Matches 26; Conservative
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US-10-356-861-142
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                 Mast, Andrea L.
Brow, Mary Ann D.
TITLE OF INVENTION: Decetion Of Nucleic Acids By Multiple
Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 550;
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 128; DB 13;
Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/350,597
FILING DATE: 09-Jul-1999
APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/758,314
FILING DATE: 29-NOV-1996
FILING DATE: 29-NOV-1996
FILING DATE: 29-NOV-1996
FILING DATE: 29-NOV-1996
APPLICATION NUMBER: US 08/55,386
FILING DATE: 29-NOV-1996
APPLICATION NUMBER: US 08/59,491
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02736
TELEPHONE: (415) 705-8410
TELEPRAX: (415) 397-838
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
Lyamichev, Victor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 550 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 92.9
Matches 26; Conservative
                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-033-297-142
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Gaps

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Indels

Length 550;

Score 128; DB 14; Pred. No. 2.8e-10;

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Sequence 142. Application US/10356861

Publication No. US20040072182A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Neri, Bruce P.
APPLICANT: Lukowiak, Andrew A.
APPLICANT: Lukowiak, Andrew A.
TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences FILE REFERENCE: FORS-07813

CURRENT APPLICATION VUMBER: 2003-02-03

NUMBER OF SEQ ID NOS: 254

SOFTWARE: Patentin version 3.2

SEQ ID NO 142

LENGTH: 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match . 93.4%; Score 128; DB 15; Best Local Similarity 92.9%; Pred. No. 2.8e-10; Matches 26; Conservative 1; Mismatches 1;
                                 345 LKQLDAQQTQLRIDSFFRLAQQEKEDAK 372
1 LKOLDAQQTQLRIDSFFRLAQQEKEDKR 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic
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Gaps

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1; Indels

1; Mismatches

345 LKQLDAQQTQLRIDSFFRLAQQEKEDAK 372

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RESULT 3
US-10-290-386-142
; Sequence 142, Application US/10290386
; Publication No. US20030152971A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Neri, Bruce P.

Neri, Bruce P. Hall, Jeff G.

APPLICANT:

1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28

345 LKQLDAQQTQLRIDSFFRLAQQEKEDAK 372

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APPLICANT: Hall, Jeff G.
Lyamichev, Victor I.
Mast, Andrea L.
Brow, Mary Ann D.
TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.4%; Score 128; DB 16; Length 550; 92.9%; Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/758,314
FILING DATE: 22-DEC-1996
APPLICATION NUMBER: US 08/756,386
FILING DATE: 22-NOV-1996
APPLICATION NUMBER: US 08/56,386
FILING DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/699,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-03295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-JAN-1996
APPLICATION NUMBER: US 08/823,516
FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/897,793
FILING DATE: 23-011-2004
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: procesin
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
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US-10-897-793-142
; Sequence 142, Application US/10897793
; Publication No. US20050003432A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 550 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 142
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Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OXIGNED Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 90 204 205 MILE
GURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                             APPLICANT: Allawi, Hatim T.
APPLICANT: Kaiser, Michael W.
APPLICANT: Ma, Wu-Po
APPLICANT: Meri, Bruce P.
APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Endonuclease-Substrate Complexes
FILE REPRENCE: FORS-08907
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 128; DB 15;
Pred. No. 6.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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Publication No. US20030044796A1
GENERAL INFORMATION:
APPLICANT: Nori, Bruce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 LKQLDAQQTQLRIDSFFRLAQQEKEDAK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
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; Sequence 143, Application US/10783557; Publication No. US20050048527A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51, Application US/10341434
Publication No. US20030215835A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 533
SOFTWARE: Patentin version 3.2
SEQ ID NO 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.4%;
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Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Conservative
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                                                                                                                                                                                                                                                                                                                                      LENGTH: 550
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-783-557-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-341-434-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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US-10-356-861-143
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Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.3%; Score 110; DB 10; Length 543; Best Local Similarity 78.6%; Pred. No. 1.2e-07; Matches 22; Conservative 3; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: <u >unknown><u >uuknown><u >uuknown><u >uukno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION: COURTION: CLIARADOWING TO APPLICATION NUMBER: US/09/350,597 FILING DATE: 09-701-1999 APPLICATION NUMBER: US/08/823,516 FILING DATE: 24-MAR-1997 APPLICATION NUMBER: US/08/759,038 FILING DATE: 21-3AN-1997 APPLICATION NUMBER: US/08/759,038 FILING DATE: 02-DEC-1996 APPLICATION NUMBER: US/08/756,386 FILING DATE: 29-NOV-1996 APPLICATION NUMBER: US/08/59,491 FILING DATE: 24-JAN-1996 APPLICATION NUMBER: US/08/59,491 FILING DATE: 22-JAN-1996 APPLICATION NUMBER: US/08/59,491 FILING DATE: 24-JAN-1996 ATTORNEY AGGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLONAUL, TOTALLE DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02736
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 LKHLNAHQTQLRIDSFFRLAQQEKQDAK 372
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Lyamichev, Victor I.
Mast, Andrea L.
Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 143, Application US/10033297
Publication No. US20020187486A1
GENERAL INFORMATION:
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 143
LENGTH: 543
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                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus musculus
US-09-940-244-143
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APPLICANT: Hall, Jeff G.
APPLICANT: Lukowiak, Andrew A.
TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences
FILE REFERENCE: FORS-07459
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                                                                                                                                                                                                                             3; Indels
STRANDEDNESS: NO. US20020187486A1 Relevant
TOPOLOGY: NO. US20020187486A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 143:
US-10-033-297-143
                                                                                                                                                                      Score 110; DB 13;
Pred. No. 1.2e-07;
3; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/10/290,386

CURRENT FLING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: 60/361,060

PRIOR FILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-15

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1996-07-09

PRIOR PILING DATE: 1996-07-09

PRIOR PILING DATE: 1996-07-09

PRIOR FILING DATE: 1996-01-26

PRIOR FILING DATE: 1996-01-24

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PATCHTIN VUMBER: 08/599,491

PRIOR FILING DATE: 1996-01-24

NUMBER OF SEQ ID NOS: 253

LENGTHAE: 543
                                                                                                                                                                                                                                                                                                               1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 143, Application US/10290386 Publication No. US20030152971A1 GENERAL INFORMATION: APPLICANT: Lyamichev, Victor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 143, Application US/10356861 Publication No. US20040072182A1 GENERAL INFORMATION:
                                                                                                                                                                      Query Match 80.3%;
Best Local Similarity 78.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Synthetic US-10-290-386-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.3
Best Local Similarity 78.6
Matches 22; Conservative
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TYPE: PRT
ORGANISM: Xenopus laevis
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Best Local Similarity
Matches 22; Conserv
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LENGTH: 527
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                    APPLICANT: Neri, Bruce P.
APPLICANT: Hall, Jeff
APPLICANT: Hall, Jeff
APPLICANT: Lukowiak, Andrew A.
TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences
FILE REFERENCE: FORS-07813
CURRENT APPLICATION NUMBER: US/10/356,861
CURRENT FILING DATE: 2003-02-03
NUMBER OF SEQ ID NOS: 254
SOFTWARE: PatentIn version 3.2
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Sequential Invasive Cleavages
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 80.3%; Score 110; DB 15; Length 543; Best Local Similarity 78.6%; Pred. No. 1.2e-07; Matches 22; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/897,793
FILING DATE: 23-JUL-2004

CLASSIFICATION: «Unknown-
PRIOR APPLICATION NUMBER: PCT/US97/01072

FILING DATE: 21-JAN-1997

APPLICATION NUMBER: US 08/759,038

FILING DATE: 20-DEC-1996

APPLICATION NUMBER: US 08/759,314

FILING DATE: 29-DEC-1996

APPLICATION NUMBER: US 08/756,386

FILING DATE: 29-NOV-1996

APPLICATION NUMBER: US 08/56,386

FILING DATE: 12-JUL-1996

APPLICATION NUMBER: US 08/682,853

FILING DATE: 12-JUL-1996

APPLICATION NUMBER: US 08/682,853

FILING DATE: 12-JUL-1996

APPLICATION NUMBER: US 08/682,853
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APPLICATION NUMBER: US 08/823,516
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INPORMATION:
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Publication No. US20050003432A1
GENERAL INFORMATION:
APPLICANT: Hall, Jeff G.
Lyamichev, Victor I.
Mast, Andrea L.
Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic US-10-356-861-143
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APPLICANT: Victor, Lyamichev
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                                                                                                                                                                                                                                             SEQ ID NO 143
LENGTH: 543
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Publication No US20050048527A1

GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Ma, Wu-Po
APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Endonuclease-Substrate Complexes
FILE REFERENCE: FORS. 08907
CURRENT APPLICATION NUMBER: US/10/783,557

CURRENT PILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 533

SOFTWARE: Patentin Version 3.2

SEQ ID NO 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 110; DB 17;
Pred. No. 1.2e-07;
3; Mismatches 3;
                    TELEPHONE: (415) 705-8410
TELEFAX: (415) 377-8338
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 anino acida
TYPE: anino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 143:
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APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION WIDBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PatentIn version 3.1
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Publication No. US20030044796A1
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION TELEPHONE: (415) 705-841
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ilarity 78.6%;
Conservative
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Best Local Similarity 78.61
Matches 22, Conservative
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CORGANISM: Mus musculus
US-10-783-557-144
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US-10-033-297-144

Sequence 144, Application US/10033297

Sequence 144, Application US/10033297

Publication No. US20020187486A1

GENERAL INFORMATION:

Jyamichev, Victor I.

Mast, Andrea L.

Brow, Mary Ann D.

TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple

Sequential Invasive Cleavages
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                                                                                      Query Match 70.1%; Score 96; DB 10; Length 527; Best Local Similarity 87.0%; Pred. No. 1.3e-05; Matches 20; Conservative 1; Mismatches 2; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STRATE: 221 fornia
COINTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/033.297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
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CLASSIFICATION 
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TOPOLOGY: No. US20020187486A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 144:
US-10-033-297-144
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**PILING DATE: 09-Jul-1999

**APPLICATION NUMBER: US/08/823,516

**FILING DATE: 20-Jul-1999

**APPLICATION NUMBER: US/08/759,038

**FILING DATE: 21-Jul-1997

**APPLICATION NUMBER: US 08/759,038

**FILING DATE: 02-DEC-1996

**APPLICATION NUMBER: US 08/756,386

**FILING DATE: 29-NOV-1996

**APPLICATION NUMBER: US 08/756,386

**FILING DATE: 29-NOV-1996

**APPLICATION NUMBER: US 08/756,386

**FILING DATE: 29-NOV-1996

**APPLICATION NUMBER: US 08/59,491

**FILING DATE: 24-Jul-1996

**APPLICATION NUMBER: US 08/59,491

**FILING DATE: 24-Jul-1996

**APPLICATION NUMBER: US 08/599,491
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REFERENCE/DOCKET NUMBER: FORS-02736
                                                                                                                                                                                                                                                                                                                           345 LKQLNAQQTQLRIDSFFRLEQHE 367
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TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acida
TYPE: amino acid
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TELEFAX: (415) 397-83:
INFORMATION FOR SEQ ID NO: 144:
US-09-940-244-144
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70.1%; Score 96; DB 13; Length 527; 87.0%; Pred. No. 1.3e-05; Live 1; Mismatches 2; Indels
   Query Match
Best Local Similarity 87.05
Matches 20; Conservative
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Search completed: May 20, 2005, 11:14:48 Job time : 1937 secs

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Local Similarity
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Q9vj84
Q9maa8
Q9maa8
Q9st35
Q7a0k3
Q7a4v5
Q6g892
Q6gf13
Q9ttux9
Q9ttux9
Q8dav8
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Q51063
Q25554
Q9xt06
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                            1 LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                1612378 segs, 512079187 residues
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XPG XENLA
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Q51063
Q25554
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Q7A0K3
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O8DAV8
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Query
Match 1
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                                   OM protein
                                                                                             Sequence:
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pseudomonas
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arabidopsis
                                                                                                                                                                                                                                            homo sapien
    acinetobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain parietal lobe;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO47633; BAB12157.1;
HSSP; O93634; 1B43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Carcopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
06f978
07pz80
05j544
06j524
09i321
088b21
09nkp9
08kvr8
045799
0844g8
0784d8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. — SEQUENCE 415 AA; 46951 MW; A861857142E340BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 0004519; E: nucleus; IEA.
GO; GO: 0004519; F: nucleus; IEA.
GO; GO: 0004519; F: single-etranded DNA binding; IEA.
GO; GO: 0005289; F: single-etranded DNA binding; IEA.
GO; GO: 0005289; F: single-etranded DNA binding; IEA.
GO; GO: 0005289; F: single-etranded DNA binding; IEA.
InterPro; IPR00918; 5_3_exo_C.
InterPro; IPR001014; XPG_DNA_repair.
InterPro; IPR001044; XPG_T.
InterPro; IPR006084; XPG_T.
PRINTS; PR000867; XRG_T.
PRINTS; PR000867; XRG_T.
PRINTS; PR000867; XRG_T.
SWART; SM00279; HHHZ; 1.
SWART; SM00279; HHHZ; 1.
SWART; SM00279; HHHZ; 1.
PROSTIE; PS00484; XPG_T.
PROSTIE; PS00484; XPG_T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.4%; Score 128; DB 2; I
llarity 92.9%; Pred. No. 1.2e-09;
Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                      415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APG HUMAN STANDARD, PRT; 1186 AA P2875; Q722V3; QBIZL6; QBN1B7; Q9HD59; 01-APR-1993 (Rel. 25, Last sequence update)
                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKQLDAQQTQLRIDSFFRLAQQEKEDKR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                     064544
995429
091321
08821
09NKP9
045799
045799
0844G8
075094
091KV8
  Q6F978
Q7PZ80
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca.
NCBI_TaxID=9541;
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Į **X STATE ST Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; "NIEMS-SNPB, environmental genome project, NIEMS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases. MEDLINE=94019313; PubMed=8413238; Macinnes M.A., Dickson J.A., Hernandez R.R., Learmonth D., Lin G.Y., Mudgett J.S., Park M.S., Schauer S., Reynolds R.J., Strniste G.F., 05-JUL-2004 (Rel. 44, Last annotation update)
MA-repair protein complementing XP-G cells (Xeroderma pigmentosum group G complementing protein) (DNA excision repair protein ERCC-5) Name=ERCC5; Synonyma=XPG, XPGC; MEDLINE=94173288; PubMed=7510366; DOI=10.1016/0921-8777(94)90080-9; Baloni T., Harada Y.-N., Saito T., Shiomi N., Okuno Y., Yamaizumi M "An ERCCS gene with homology to yeast RAD2 is involved in group G Xeroderma pigmentosum."; Scherly D., Nouspikel T., Corlet J., Ucla C., Bairoch A., Clarkson S.G.; "Complementation of the DNA repair defect in Xeroderma pigmentosum group G cells by a human cDNA related to yeast RAD2."; Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. "Human ERCC5 cDNA-cosmid complementation for excision repair and bipartite amino acid domains conserved with RAD proteins of Saccharomyces cerevisiae and Schizosaccharomyces pombe."; Mol. Cell. Biol. 13:6393-6402(1993). SEQUENCE FROM N.A., AND VARIANT ASP-1104.
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Nucleic Acids Res. 29:1443-1452(2001). TISSUE=Bone marrow; Zan Q., Guo J.H., Yu L.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. MEDLINE=93247645; PubMed=8483504; DOI=10.1038/363182a0; group G cells by a human cDNA related to yeast RAD2."; Nature 363:182-185(1993). SEQUENCE FROM N.A., AND VARIANTS VAL-254 AND ASP-1104 SEQUENCE FROM N.A., AND VARIANT ASP-1104. SEQUENCE FROM N.A., AND VARIANT ASP-1104. Mutat. Res. 314:167-175(1994). SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxID=9606; Homo sapiens

full-length human unicanciator with Turk.

PubMed=9305916; DOI=10.1074/jbc.272.39.24522;

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Gary R., Edwig D.L., Cornellus H.L., MacInnes M.A., Park M.S.;

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MEDLINE=94375034; PubMed=8088806;
Samec S., Jones T.A., Corlet J., Scherly D., Sheer D., Wood R.D.
Clarkson S.G.; "The human gene for Xeroderma pigmentosum complementation group (XPG) maps to 13q33 by fluorescence in situ hybridization."; Genomics 21:283-285 (1994). MEDLINE=94376899; PubMed=8090225; DOI=10.1038/371432a0; O'Donovan A., Davies A.A., Moggs J.G., West S.C., Wood R.D.; "XPG endonuclease makes the 3' incision in human DNA nucleotide PubMed=7651464; DOI=10.1016/0165-7992(95)90070-5; Cloud K.G., Shen B., Strniste G.F., Park M.S., "XPG protein has a structure-specific endonuclease activity."; Mutat. Res. 347:55-60(1995). MEDLINE-95038755; PubMed=7951246; Nouspikel T., Clarkson S.G.; "Mutations that disable the DNA repair gene XPG in a Xeroderma a DNA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) PubMed=14726017; DOI=10.1016/j.biochi.2003.10.014; Habraken Y., Sung P., Prakash L., Prakash S.; "Human Xeroderma pigmentosum group G gene encodes CHARACTERIZATION, AND SUBCELLULAR LOCATION. VARIANT XP-G VAL-792, AND VARIANT ASP-1104 Nucleic Acids Res. 22:3312-3316(1994). J. Biol. Chem. 269:15965-15968(1994). CHARACTERIZATION. MEDLINE=94266772; PubMed=8206890; MEDLINE=94359802; PubMed=8078765; pigmentosum group G patient."; Hum. Mol. Genet. 3:963-967(1994). Biochimie 85:1113-1121(2003). Nature 371:432-435(1994). REVIEW ON VARIANTS XP-G INTERACTION WITH PCNA. VARIANT XP-G VAL-792 CHARACTERIZATION. CHARACTERIZATION. endonuclease."; excision repair Clarkson S.G.; "The XPG story endonuclease. REVIEW

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PRINTS; PR00853; XPGRADSUPER
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MEDLINE=22055379; PubMed=12060391;

MEDLINE=22055379; PubMed=12060391;

Emmert S., Slor H., Busch D.B., Barko S., Albert R.B., Coleman D.,

Khan S.G., Abu-Libdeh B., Didiovanna J.J., Cunningham B.B., Lee M.M.,

Crollick J., Inui H., Ueda T., Hedayati M., Grossman L., Shahlavi T.,

A Creaver X.B.,

"Relationship of neurologic degeneration to genotype in three

recoderma pigmentosum group G patients.",

J. Invest. Dermatol. 118:972-982 (2002).

J. Invest. Dermatol. 118:972-982 (2002).

J. Invest. Dana excision repair. (MRR). Acts as a cofactor for a DNA nucleotide excision repair. (MRR). Acts as a cofactor for a DNA glycosylase that removes oxidised pyrimidines from DNA. May also be involved in transcription by RNA polymerase II, and perhaps in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (psychomotor retardation, deafness, optic atrophy, retinal pigmentation and hyperreflexes), and dysmorphic dwarfism (immature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other processes too.

SUBUNIT: Interacts with PCNA.
SUBCELLULAR LOCATION: Nuclear.

DISEASE: Defects in ERCC5 are the cause of xeroderma pigmentosum complementation group G (XP-G) [MIM:278870]; also known as xeroderma pigmentosum VII (XP7). XP-G is an autosomal recessive disease characterized by hypersensitivity of the skin to sunlight followed by high incidence of skin cancer and frequent neurologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recessive disease
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                                                                                                     MEDLINE=21126776; PubMed=11228268; Zafeiriou D.I., Thorel P., Andreou A., Kleijer W.J., Raams A., Garritesn V.H., Gombakis N., Jaspers N.G.J., Clarkson S.G.; "Acroderma pigmentosum group G with severe neurological involvement and features of Cockayne syndrome in infancy."; Pediatr. Res. 49:407-412(2001).
                                                                                                                                                                                                                                                                          VARIANT XP-G PRO-858.
MEDLINE=21830955; PubMed=11841555;
Lalle P., Nouspikel T., Constantinou A., Thorel F., Clarkson S.G.;
Lathe founding members of xeroderms pigmentosum group G produce XPG
procesin with severely impaired endonuclease activity.";
J. Invest. Dermatol. 118:344-351(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pigmentation abnormalities), neurological dysfunction due to demyelination of neurons and calcification of basal ganglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XPG MOUSE STANDARD; PRT; 1170 AA.
P35689; Q61528; Q64248;
01-JUN-1994 (Rel. 29, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
DNA-repair protein complementing XP-G cells homolog (Xeroderma pigmentosum group G complementing protein homolog) (DNA excision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: Defects in ERCC5 are one of the cause of Cockayne' syndrome (CS) [MIM:216400]. CS is an autosomal recessive diwhich is characterized by a UV-sensitive skin (without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
  Xeroderma pigmentosum group G: implications for a second XPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.4%; Score 128; DB 1; Length 1186; ilarity 92.9%; Pred. No. 3.8e-09; Conservative 1; Mismatches 1; Indels
                                              roc. Natl. Acad. Sci. U.S.A. 94:3116-3121(1997).
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Name=Ercc5, Xpg;
                                                                                            VARIANT XP-G/CS HIS-72.
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                          unction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic XPG gene...;

Mamm. Genome 7:644-649(1996).

-!- PUNCITION: Single-stranded structure-specific DNA endonuclease
involved in DNA excision repair. Makes the 3'incision in DNA
nucleotide excision repair (NER). Acts as a cofactor for a DNA
glycosylase that removes oxidised pyrimidines from DNA. May also
be involved in transcription-coupled repair of this kind of
damage, in transcription by RNA polymerase II, and perhaps in
other processes too (By similarity).
-!- SUBGNIT: Interacts with PCNA (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the XPG/RAD2 endonuclease family. XPG
                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/10; TISSUE=Liver;
MEDLINE=96070433; PubMed=7590748;
Harada Y.N., Matsuda Y., Shiomi N., Shiomi T.;
"Complementary DNA sequence and chromosomal localization of xpg, the mouse counterpart of human repair gene XPG/ERCC5.";
Genomics 28:59-65(1995).
                                                                                                                          MEDLINE-94173288; PubMed-7510366; DOI-10.1016/0921-8777(94)90080-9; Shiomi T., Harada Y.-N., Saito T., Shiomi N., Okuno Y., Yamaizumi M "An ERCC5 gene with homology to yeast RAD2 is involved in group G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and structural analysis of the functional mouse
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96359149; Pubmed=8703115;
Ludwig D.L., Mudgett J.S., Park M.S., Perez-Castro A.V.,
Macinnes M.A.;
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Interpro; IPR001044; XPGC_DNA_repair.
Interpro; IPR006084; XPGC_Rad_
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U40795; AAB17885.1; -.
U39892; AAB17885.1; JOINED.
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U39894; AAB17885.1; JOINED.
U39896; AAB17885.1; JOINED.
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                                                                                                                                                                                                                                Xeroderma pigmentosum.";
Mutat. Res. 314:167-175(1994).
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InterPro; IPR000513; Exo N I.
InterPro; IPR006086; XPG I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D16306; BAA03813.1; -.
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1040073; AAB17885.1; U
1040432; AAB17885.1; U
1040669; AAB17885.1; U
1040669; AAB17885.1; U
10406792; AAB17885.1; U
1040792; AAB17885.1; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U40793; AAB17885.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A57650; A57650.
MGD; MGI:103582; Ercc5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00867; XPG
Pfam; PF00752; XPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=DBA/2;
                                                                                                                                                                                                                                                                                                                            SEQUENCE
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TISSUE=Embryo;
PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1014 LKQLNAQQTQLRIDSFFRLEQHE 1036
                                                                                                                                                                                                                                                                                                                                    DNA repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKOLDACOTOLRIDSFFRLACOE 23
                                                                                                                                                                                                                                            InterPro; IPR008918; 5.3 exo_C.
InterPro; IPR008918; 8xo_N I.
InterPro; IPR006086; XPG_I.
InterPro; IPR006086; XPG_N.
InterPro; IPR001044; XPGC_DNA_rep
InterPro; IPR006084; XPGC_Rad_
Pfam; PF00867; XPG_I.
Pfam; PF00867; XPG_N; I.
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0853; XPGRADSUPER.
PRINTS; PRO0066; XRODRMEGNNTG.
SMART; SMO0279; HHHZ; 1.
SMART; SMO0484; XPGI; 1.
SMART; SMO0485; XPGI; 1.
                                                                                                                                                                                                           EMBL; X69977; CAA49597.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 70.1%;
Local Similarity 87.0%;
es 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1095
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786 91
936 95
1079 109
                                                                                                                                                                                                                                 PIR; S35994; S35994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complementation of the DNA repair defect in Xeroderma pigmentosum group G cells by a human CDNA related to yeast RAD2.";
Nature 363:182-1865 [1933].

-1- FUNCTION: Single-stranded structure-specific DNA endonuclease involved in DNA excision repair. Makes the 3'incision in DNA nucleotide excision repair (NER). Acts as a cofactor for a DNA glycosylase that removes oxidised pyrimidines from DNA. May also be involved in transcription-coupled repair of this kind of damage, in transcription by RNA polymerase II, and perhaps in other processes too (By similarity).
-1- SUBCELDIAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                               Nuclear localization signal (Potential)
                                                                           TICRFAMS; TIGRO0600; rad2; 1.
PROSITE; PS00841; XPG_1; 1.
PROSITE; PS00842; XPG_2; 1.
DNA repair; DNA-binding; Endonuclease; Hydrolase; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pigmentosum group G complementing protein homolog).
Name-ERCC5; Synonyms-XPG, XPGC;
Nenpous laevis (African clawed frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
NA-repair protein complementing XP-G cells homolog (Xeroderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.3%; Score 110; DB 1; Length 1170; 78.6%; Pred. No. 1.3e-06; Live 3; Mismatches 3; Indels
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MEDLINE=91247645; PubMed=8483504; DOI=10.1038/363182a0;
Scherly D., Nouspikel T., Corlet J., Ucla C., Bairoch A.,
Clarkson S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> M (in Ref. 1).
-> DVQTGG (in Ref. 1).
-> NSASEVIGPV (in Ref. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> V (in Ref. 1).
-> AMEKEFEL (in Ref. 1).
                                                                                                                                                                                                                                            R -> C (in strain DBA/2).
S -> R (in strain DBA/2).
S -> N (in strain DBA/2).
S -> N (in strain DBA/2).
M -> I (in strain DBA/2).
N -> M (in Ref. 1).
N -> NSASEVIGPV (in Ref. 1).
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S -> SD (i
KL -> RR (
    XRODRMPGMNTG.
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                 SMART; SM00279; HhH2; 1.
SMART; SM00484; XPGI; 1.
SMART; SM00485; XPGN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1158
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NCBL_TaxID=8355;
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ses 22, Conserv
PR00066;
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P14629;
                                                                                                                                                                   Muclease.
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CONFLICT
SEQUENCE
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VARIANT
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VARIANT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear localization signal (Potential).
Nuclear localization signal (Potential).
My IPICE1891A3C0623 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR00600; rad2; 1.
PROSITE; PS00841; XPG_1; 1.
PROSITE; PS00842; XPG_2: 1.
DNA repair; DNA-binding; Endonuclease; Hydrolase; Nuclear protein;
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 96; DB 1; Length 119
Pred. No. 0.00012;
1; Mismatches 2; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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I-domain.
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Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pama P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                             Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lieb J.M., Lin J., Miranda M., Narusaka M., Nouyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Sarou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY124880; AAM70589.1; -.
                                                                                                                                      Ecker J.R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00560; LRR 1; 7.
PRINTS; PR00019; LEGRIYPT.
SMART; SM0369; LRR TYP; 11.
SEQUENCE 464 AA; —51647 MW; DBE6F7D9FB7C4A4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.2;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.8%; Score 60;
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InterPro; IPR003591; LRR_typ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.08;
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Matches 13; Conservative
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
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es 13; Conserv
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Pfam; PF00560; LRR
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Name=F13K23.23;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hoppins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., An Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzuy D.M., Sodergren B.J., Lu X., Gibbs R.A., An Helton B., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Makelley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; """ "Generation and initial analysis of more than 15,000 full-length human and many and montes only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryots, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 70.1%; Score 96; DB 2; Length 1197; 1 Similarity 87.0%; Pred. No. 0.00012; 20; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGRUUDOU, - TIGRUSOUS, - TIGREAMS; TIGRUUDOU, - TIGRES TIS, ESOUGH1; XPG 1; 1.
PROSITE; PSO0642; XPG 2; 1.
PROSITE; PSO0642; AA; 134331 MW; 99A9988C8CDB3711 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BCO7365; AAH77363.1; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005639; F:nucleus; IEA.
GO; GO:0005691; F:single-stranded DNA binding; IEA.
GO; GO:0006289; P:nucleotide-excision repair; IEA.
InterPro; IPR006318; 5.3 exo.C.
InterPro; IPR006318; 5.3 exo.C.
InterPro; IPR00638; XPGC_RAG.
InterPro; IPR006084; XPGC_RAG.
InterPro; IPR006084; XPGC_RAG.
InterPro; IPR006086; XPG_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
At1g12970/P13K22_18.
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PRINTS; PR00066; XRODRMPGMNTG.
                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
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SMART; SM00484; XPGI; 1.
SMART; SM00485; XPGN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Best Local (
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Gaps

5

6; Indels

Length 464;

DB 2;

RAPARA RA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
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Last sequence update)
Last annotation update)
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50.0%; Pred. No. 5.6;
iive 5; Mismatches 6
                                                                                                                                                                           492 AA
                                    350 LRELDLSNNQIRVLPDSFFRLEKLEK 375
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RESULT 6

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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
MEDLINES-9449929; PubMed=80704009;
MEDLINES-944992929; PubMed=80704009;
Ireland L.S., Johnston G.C., Drebot M.A., Dhillon N., Demaggio A.J.,
Hoekstra M.F., Singer R.A.;
Hoekstra M.F., Singer R.A.;
Ha member of a novel family of yeast 'Zn-finger' proteins mediates the
transition from stationary phase to cell proliferation.";
EMBO J. 13:3812-3821(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99126358; PubMed=9927415; DOI=10.1093/emboj/18.3.555; Poon P.P., Cassel D., Spang A., Rotman M., Pick E., Singer R.A., Johnston G.C.; "Retrograde transport from the yeast Golgi is mediated by two ARF GAP proteins with overlapping function."; EMBO J. 18:555-564(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 18:555-564(1999).
-!- FUNCTION: Involved in transition from stationary to proliferative
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C / AB972;
MEDLINE=97313264; PubMed=9169868;
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
Cherry J.M., Chung E., Buncan M., Guzman E., Hartzell G.,
Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Golgi stack; GrPase activation; Protein transport; Transport; Zinc-finger.

DOMAIN 15 137 Arf-GAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X79514; CAA56046.1; -.

EMBL; U18916; AAC3220.1; -.

EMBL; U18916; AAC3220.1; -.

Germonline; 139201; -.

GGD; S00000924; GLO3.

GO; GO:0008060; F:RR-GOlgi intermediate compartment; IPI.

GO; GO:0008889; P:RR GTPase activator activity; IDA.

GO; GO:0006889; P:RR to Golgi transport; IGI.

GO; GO:0006889; P:RR to Golgi transport; Golgi to ER; IDA.

HIGEPEPO; ARGOLGI intermediate Compartment; IPI.

GO; GO:0006889; P:RR to Golgi transport; Golgi to ER; IDA.

HIGEPEPO; ARGOLGI interportate transport, Golgi to ER; IDA.
                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
ADP-ribosylation factor GTPase-activating protein GLO3
                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                               493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 Arf-GAP domain.
                                                                                                                                                            Name=GLO3; OrderedLocusNames=YER122C;
                                                               PRT;
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PRINTS; PR00405; REVINTRACTNG.
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PROSITE; PS50115; ARFGAP;
                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 387:78-81(1997)
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                            GLO3 YEAST
P38682;
                               RESULT 8
GLO3_YEAST
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In Nature 0:0.0 (2003).
C4-type.
S -> C (in Ref. 1). FGEDKEVDEFGNPINSSGSGA EAHDKIKTPDNATSISSSYFGEDKEVDEFGNPINSSGSGA GNFDGRNSNNGFIDFNASADDELQMIRDVVEQGAEKLGSYL RDYLRK -> GSA (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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                                                                                                                                                                                      DB 1; Length 493;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypochetical protein.
SROUTENCE 2097 AA; 232292 MW; 470AF47EB082BFA5 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2097 AA
                                                                                                                                                                                                               46.2%; Pred. No. 15;
cive 5; Mismatches
                                                                                                                                                                                         Score 57;
                                                                                                                                                                                                                                                                                                                               2 KOLDAQOTQLRIDSFFRLAQQEKEDK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866 KEFDAÇOYOKRIDELTTMISOVKEE 890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
EMBL; AABX01000718; EAA28438.1;
                                                                                                                                        55093 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Related to nucleoprotein TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Hypotherical protein. Name=NCU04059.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 48.0%;
Matches 12; Conservative
                                                                                                                                                                                            41.68;
                                                                                                                                                                                      Query Match
Best Local Similarity 46.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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          54
222
493
                                                                                                                                        493 AA;
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          31
222
406
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                                                                                                                                        SEQUENCE
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REAL MEDILINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Addams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocapte J.D., RA MEDILINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Amanatides P.G., Scherer S.E., Li P.W., Holskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S.P., Ashburner M., Henderson S.N., Burandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Ann K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pénnhoch C.R., Baddwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Bensen K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Brottler P., Borchan M.R., Boukova D., Botchan M.R., Bouck J., Brokstein P., Brottler B., Botchan M.R., Bourson D.A., Buller H., Cadleu E., Center A., Chandra I., RA Gebon K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Burtis K.C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Andrews D., Botchar A., Garjelista C.C., Ferraz C., Ferriera S., Plaison B., Blain M., Kalush F., Karpen G.H., Ke Z., Gulbar W.M., Glasser K., Alashi M., Kalush F., Karpen G.H., Ke Z., Gulbar W.M., Glasser K., Alashi M., Kalush F., Karpen G.H., Ke Z., Gulbar W.M., Glasser M.G., Lasko P., Lei Y., Levitsky A.A., Li J., U. Z., Liang Y., Lin X., Mattei B.., McIntosh T.C., McIeod M.P., Morphy L., Moy M., Nelson D.L., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Alazon D., Rahmen B.E., Rodira C.D., Kraft C., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Gelniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
                 Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002)
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                                                                                                                                                              Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantee, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi B., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J. M., Liu S., Mikharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
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                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 2; Length 2115;
Pred. No. 98;
3; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            5D44A9B0A9FE537C CRC64;
                                                                                                                                                                                                                                                                                 German Neurospora genome project;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
EMBL, BX897679; CAE85613.1;
GO; GO:0019013; C:viral nucleocapsid; IEA.
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Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.9%;
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SEQUENCE 368 AA; 42510 !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 48.0
les 12; Conservative
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                         Neurospora crassa.
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                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                            NCBI_TaxID=5141;
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Name=B2C22.040;
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09FX50

Matches

8 \$

RESULT 11
09FX50
10 09FX5
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DT 01-MA
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Q9VJ84 Q9VJ84;

22444B

Matches

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Nature 415:871-880(2002)
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REDIINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

REDIINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

REDIINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

REDIINE=21848401; Payles J., Basham D., Bowman S.,

REDIINES M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

REDIINES M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

REDIINES M., Onnor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,

RA HOLYOYG S., Hornbay T., Howarth S., McDonald S., McLean J.,

RA HOLYOYG S., Mongall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Molver K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

B. Geffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Ra Lucas M., Rochet M., Gaillardin C., Pallada V., Garzon A., Thode G.,

Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Dominguez A., Revuelta J.L., Moreno S., Amarstrong J., Forsburg S.L.,

Dominguez A., Revuelta J.L., Moreno S., Amarstrong J., Forsburg S.L.,

A Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";
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Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                       Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 730;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases EMBL, AE003659; AAF53670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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Intac; 909/084; -.
FlyBase, FBgn0032681; CG10283.
FlyBase, FBgn0032681; CG10283.
FlyBase, FBgn0032681; CG10283.
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                               systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Putative proteasome maturation factor umpl.
ORFNames=SPCC14G10.03c;
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Pred. No. 70;
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Best Local Similarity 44.0%;
Matches 11; Conservative
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074416;
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-i- FUNCTION: Short-lived chaperone present in the precursor form of
the 20S proteasome and absent in the mature complex. Required for
the correct assembly and enzymatic activation of the proteasome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĸ
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М.Е.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 129;
13;
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Chaperone; Hypothetical protein; Proteasome.
SEQUENCE 129 AA; 14661 MW; 36CAE66B313BE4C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.7%; Score 53; DB 41.9%; Pred. No. 40; ive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                           EMBL; AL031518; CAA20656.1; -.
                                                                                                                                                                                                                                                                                                                                             PIR, T41014; T41014.
GeneDB_SPombe; SPCC14G10.03c;
InterPro; IPR008012; UMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24, Hypothetical protein. OrderedLocusNames=SAV1843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 39...,
Local 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 41.9<sup>*</sup>
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                               (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF05348; UMP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T12H1.7 protein.
Name=T12H1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9MAA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q99T35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99T35
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STRAIN=MUSO, ATCC 700699;
STRAIN=MUSO, ATCC 700699;
STRAIN=MUSO, ATCC 700699;
MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.0%; Score 52; DB 2; Length 978; Best Local Similarity 45.5%; Pred. No. 1.6e+02; Matches 15; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                 Lancet 357:1225-1240(2001).

EMBL, AP003363; BAB58005.1; -.
PIR; B89971; B89971.

Complete proteome; Hypothetical protein.

SEQUENCE 978 AA; 114404 MW; A41F40B086E98BC2 CRC64;
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=158878;
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Search completed: May 20, 2005, 10:26:17 Job time : 59 secs

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